(1) GENERAL INFORMATION:

   (i) APPLICANT: Reed, John

   (ii) TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

 (iii) NUMBER OF SEQUENCES: 29

  (iv) CORRESPONDENCE ADDRESS:
     (A) ADDRESSEE: LONG, ALDRIDGE & NORMAN LLP

     (B) STREET: Suite 600, 701 Pennsylvania Avenue, N.W.
     (C) CITY: Washington
     (D) STATE: District of Columbia
     (E) COUNTRY: U.S.A.
     (F) ZIP: 20004

   (v) COMPUTER READABLE FORM:
     (A) MEDIUM TYPE: Floppy disk
     (B) COMPUTER: IBM PC compatible
     (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

  (vi) CURRENT APPLICATION DATA:
     (A) APPLICATION NUMBER: US 08/465,485
     (B) FILING DATE: 05-JUN-1995
     (C) CLASSIFICATION:

 (vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: US 08/124,256
     (B) FILING DATE: 20-SEP-1993

 (vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: US 07/840,716
     (B) FILING DATE: 21-FEB-1992

 (vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: US 07/288,692
     (B) FILING DATE: 22-DEC-1988

(viii) ATTORNEY/AGENT INFORMATION:
     (A) NAME: Steven B. Kelber
     (B) REGISTRATION NUMBER: 30,073
     (C) REFERENCE/DOCKET NUMBER: 3335-075-55 CONT

  (ix) TELECOMMUNICATION INFORMATION:
     (A) TELEPHONE: (202) 624-1200
     (B) TELEFAX: (202) 624-1298

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGCGTGCGC CATCCTTCCC                        20


(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTTTTCCTCT GGGAAGGATG GCGCACGCTG GGAGA          35


(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATGCACCTA CCCAGCCTCC                        20

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACGGGGTACG GAGGCTGGGT AGGTGCATCT GGT           33


(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAAAGGCAT CCTGCAGTTG           20


(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCCCAACTG CAGGATGCCT TTGTGGAACT GTACGG           36

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGAAGGATG GCGCACGCTG                              20


(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGTGCGAC CCTCTTG                              17


(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TACCGCGTGC GACCCTC                              17

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCCTACCGCG TGCGACC                                                    17


(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCTTCCTACC GCGTGCG                                                    17


(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GACCCTTCCT ACCGCGT                                                    17

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGACCCTT CCTACCG                                 17


(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGGCGGCAG CGCGG                                 15


(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGGCGGGGCG ACGGA                                 15

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (iv) ANTI-SENSE: YES

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGGAGCGCG GCGGGC                                                    16


(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCTCCCAGCG TGCGCCAT                                                  18


(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGCACTCACG CTCGGCCT                                                  18


(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 5086 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

```
GCGCCCGCCC CTCCGCGCCG CCTGCCCGCC CGCCCGCCGC GCTCCCGCCC GCCGCTCTCC      60

GTGGCCCCGC CGCGCTGCCG CCGCCGCCGC TGCCAGCGAA GGTGCCGGGG CTCCGGGCCC     120

TCCCTGCCGG CGGCCGTCAG CGCTCGGAGC GAACTGCGCG ACGGGAGGTC CGGGAGGCGA     180

CCGTAGTCGC GCCGCCGCGC AGGACCAGGA GGAGGAGAAA GGGTGCGCAG CCCGGAGGCG     240

GGGTGCGCCG GTGGGGTGCA GCGGAAGAGG GGGTCCAGGG GGAGAACTT CGTAGCAGTC      300

ATCCTTTTTA GGAAAGAGG GAAAAAATAA AACCCTCCCC CACCACCTCC TTCTCCCCAC      360

CCCTCGCCGC ACCACACACA GCGCGGGCTT CTAGCGCTCG GCACCGGCGG GCCAGGCGCG     420

TCCTGCCTTC ATTTATCCAG CAGCTTTTCG GAAAATGCAT TTGCTGTTCG GAGTTTAATC     480

AGAAGACGAT TCCTGCCTCC GTCCCCGGCT CCTTCATCGT CCCATCTCCC CTGTCTCTCT     540

CCTGGGGAGG CGTGAAGCGG TCCCGTGGAT AGAGATTCAT GCCTGTGTCC GCGCGTGTGT     600

GCGCGCGTAT AAATTGCCGA GAAGGGGAAA ACATCACAGG ACTTCTGCGA ATACCGGACT     660

GAAAATTGTA ATTCATCTGC CGCCGCCGCT GCCAAAAAAA AACTCGAGCT CTTGAGATCT     720

CCGGTTGGGA TTCCTGCGGA TTGACATTTC TGTGAAGCAG AAGTCTGGGA ATCGATCTGG     780

AAATCCTCCT AATTTTTACT CCCTCTCCCC CCGACTCCTG ATTCATTGGG AAGTTTCAAA     840

TCAGCTATAA CTGGAGAGTG CTGAAGATTG ATGGGATCGT TGCCTTATGC ATTTGTTTTG     900

GTTTTACAAA AAGGAAACTT GACAGAGGAT CATGCTGTAC TTAAAAAATA CAAGTAAGTC     960

TCGCACAGGA AATTGGTTTA ATGTAACTTT CAATGGAAAC CTTTGAGATT TTTTACTTAA    1020

AGTGCATTCG AGTAAATTTA ATTTCCAGGC AGCTTAATAC ATTGTTTTTA GCCGTGTTAC    1080

TTGTAGTGTG TATGCCCTGC TTTCACTCAG TGTGTACAGG AAACGCACC TGATTTTTTA     1140

CTTATTAGTT TGTTTTTTCT TTAACCTTTC AGCATCACAG AGGAAGTAGA CTGATATTAA    1200

CAATACTTAC TAATAATAAC GTGCCTCATG AAATAAAGAT CCGAAAGGAA TTGGAATAAA    1260

AATTTCCTGC GTCTCATGCC AAGAGGGAAA CACCAGAATC AAGTGTTCCG CGTGATTGAA    1320

GACACCCCCT CGTCCAAGAA TGCAAAGCAC ATCCAATAAA ATAGCTGGAT TATAACTCCT    1380

CTTCTTTCTC TGGGGGCCGT GGGGTGGGAG CTGGGGCGAG AGGTGCCGTT GGCCCCCGTT    1440

GCTTTTCCTC TGGGAAGGAT GGCGCACGCT GGGAGAACGG GGTACGACAA CCGGGAGATA    1500

GTGATGAAGT ACATCCATTA TAAGCTGTCG CAGAGGGCT ACGAGTGGGA TGCGGGAGAT     1560

GTGGGCGCCG CGCCCCGGG GGCCGCCCCC GCACCGGGCA TCTTCTCCTC CCAGCCCGGG     1620

CACACGCCCC ATCCAGCCGC ATCCCGCGAC CCGGTCGCCA GGACCTCGCC GCTGCAGACC    1680
```

```
CCGGCTGCCC CCGGCGCCGC CGCGGGGCCT GCGCTCAGCC CGGTGCCACC TGTGGTCCAC    1740

CTGGCCCTCC GCCAAGCCGG CGACGACTTC TCCCGCCGCT ACCGCGGCGA CTTCGCCGAG    1800

ATGTCCAGCC AGCTGCACCT GACGCCCTTC ACCGCGCGGG GACGCTTTGC CACGGTGGTG    1860

GAGGAGCTCT TCAGGGACGG GGTGAACTGG GGGAGGATTG TGGCCTTCTT TGAGTTCGGT    1920

GGGGTCATGT GTGTGGAGAG CGTCAACCGG GAGATGTCGC CCCTGGTGGA CAACATCGCC    1980

CTGTGGATGA CTGAGTACCT GAACCGGCAC CTGCACACCT GGATCCAGGA TAACGGAGGC    2040

TGGGATGCCT TTGTGGAACT GTACGGCCCC AGCATGCGGC CTCTGTTTGA TTTCTCCTGG    2100

CTGTCTCTGA AGACTCTGCT CAGTTTGGCC CTGGTGGGAG CTTGCATCAC CCTGGGTGCC    2160

TATCTGAGCC ACAAGTGAAG TCAACATGCC TGCCCCAAAC AAATATGCAA AAGGTTCACT    2220

AAAGCAGTAG AAATAATATG CATTGTCAGT GATGTACCAT GAAACAAAGC TGCAGGCTGT    2280

TTAAGAAAAA ATAACACACA TATAAACATC ACACACACAG ACAGACACAC ACACACACAA    2340

CAATTAACAG TCTTCAGGCA AAACGTCGAA TCAGCTATTT ACTGCCAAAG GGAAATATCA    2400

TTTATTTTTT ACATTATTAA GAAAAAGAT TTATTTATTT AAGACAGTCC CATCAAAACT     2460

CCGTCTTTGG AAATCCGACC ACTAATTGCC AAACACCGCT TCGTGTGGCT CCACCTGGAT    2520

GTTCTGTGCC TGTAAACATA GATTCGCTTT CCATGTTGTT GGCCGGATCA CCATCTGAAG    2580

AGCAGACGGA TGGAAAAAGG ACCTGATCAT TGGGGAAGCT GGCTTTCTGG CTGCTGGAGG    2640

CTGGGGAGAA GGTGTTCATT CACTTGCATT TCTTTGCCCT GGGGGCGTGA TATTAACAGA    2700

GGGAGGGTTC CCGTGGGGGG AAGTCCATGC CTCCCTGGCC TGAAGAAGAG ACTCTTTGCA    2760

TATGACTCAC ATGATGCATA CCTGGTGGGA GGAAAAGAGT TGGGAACTTC AGATGGACCT    2820

AGTACCCACT GAGATTTCCA CGCCGAAGGA CAGCGATGGG AAAAATGCCC TTAAATCATA    2880

GGAAAGTATT TTTTAAGCT ACCAATTGTG CCGAGAAAG CATTTTAGCA ATTTATACAA      2940

TATCATCCAG TACCTTAAAC CCTGATTGTG TATATTCATA TATTTTGGAT ACGCACCCCC    3000

CAACTCCCAA TACTGGCTCT GTCTGAGTAA GAAACAGAAT CCTCTGGAAC TTGAGGAAGT    3060

GAACATTTCG GTGACTTCCG ATCAGGAAGG CTAGAGTTAC CCAGAGCATC AGGCCGCCAC    3120

AAGTGCCTGC TTTTAGGAGA CCGAAGTCCG CAGAACCTAC CTGTGTCCCA GCTTGGAGGC    3180

CTGGTCCTGG AACTGAGCCG GGCCCTCACT GGCCTCCTCC AGGGATGATC AACAGGGTAG    3240

TGTGGTCTCC GAATGTCTGG AAGCTGATGG ATGGAGCTCA GAATTCCACT GTCAAGAAAG    3300

AGCAGTAGAG GGGTGTGGCT GGGCCTGTCA CCCTGGGGCC CTCCAGGTAG GCCCGTTTTC    3360

ACGTGGAGCA TAGGAGCCAC GACCCTTCTT AAGACATGTA TCACTGTAGA GGGAAGGAAC    3420
```

-10-

```
AGAGGCCCTG GGCCTTCCTA TCAGAAGGAC ATGGTGAAGG CTGGGAACGT GAGGAGAGGC      3480

AATGGCCACG GCCCATTTTG GCTGTAGCAC ATGGCACGTT GGCTGTGTGG CCTTGGCCAC      3540

CTGTGAGTTT AAAGCAAGGC TTTAAATGAC TTTGGAGAGG GTCACAAATC CTAAAAGAAG      3600

CATTGAAGTG AGGTGTCATG GATTAATTGA CCCCTGTCTA TGGAATTACA TGTAAAACAT      3660

TATCTTGTCA CTGTAGTTTG GTTTTATTTG AAAACCTGAC AAAAAAAAG TTCCAGGTGT       3720

GGAATATGGG GGTTATCTGT ACATCCTGGG GCATTAAAAA AAAATCAATG GTGGGGAACT      3780

ATAAAGAAGT AACAAAGAA GTGACATCTT CAGCAAATAA ACTAGGAAAT TTTTTTTTCT       3840

TCCAGTTTAG AATCAGCCTT GAAACATTGA TGGAATAACT CTGTGGCATT ATTGCATTAT      3900

ATACCATTTA TCTGTATTAA CTTTGGAATG TACTCTGTTC AATGTTTAAT GCTGTGGTTG      3960

ATATTTCGAA AGCTGCTTTA AAAAAATACA TGCATCTCAG CGTTTTTTTG TTTTTAATTG      4020

TATTTAGTTA TGGCCTATAC ACTATTTGTG AGCAAAGGTG ATCGTTTTCT GTTTGAGATT      4080

TTTATCTCTT GATTCTTCAA AAGCATTCTG AGAAGGTGAG ATAAGCCCTG AGTCTCAGCT      4140

ACCTAAGAAA AACCTGGATG TCACTGGCCA CTGAGGAGCT TTGTTTCAAC CAAGTCATGT      4200

GCATTTCCAC GTCAACAGAA TTGTTTATTG TGACAGTTAT ATCTGTTGTC CCTTTGACCT      4260

TGTTTCTTGA AGGTTTCCTC GTCCCTGGGC AATTCCGCAT TTAATTCATG GTATTCAGGA      4320

TTACATGCAT GTTTGGTTAA ACCCATGAGA TTCATTCAGT TAAAAATCCA GATGGCGAAT      4380

GACCAGCAGA TTCAAATCTA TGGTGGTTTG ACCTTTAGAG AGTTGCTTTA CGTGGCCTGT      4440

TTCAACACAG ACCCACCCAG AGCCCTCCTG CCCTCCTTCC GCGGGGGCTT TCTCATGGCT      4500

GTCCTTCAGG GTCTTCCTGA AATGCAGTGG TCGTTACGCT CCACCAAGAA AGCAGGAAAC      4560

CTGTGGTATG AAGCCAGACC TCCCCGGCGG GCCTCAGGGA ACAGAATGAT CAGACCTTTG      4620

AATGATTCTA ATTTTTAAGC AAAATATTAT TTTATGAAAG GTTTACATTG TCAAAGTGAT      4680

GAATATGGAA TATCCAATCC TGTGCTGCTA TCCTGCCAAA ATCATTTTAA TGGAGTCAGT      4740

TTGCAGTATG CTCCACGTGG TAAGATCCTC CAAGCTGCTT TAGAAGTAAC AATGAAGAAC      4800

GTGGACGTTT TTAATATAAA GCCTGTTTTG TCTTTTGTTG TTGTTCAAAC GGGATTCACA      4860

GAGTATTTGA AAAATGTATA TATATTAAGA GGTCACGGGG CTAATTGCT AGCTGGCTGC       4920

CTTTTGCTGT GGGGTTTTGT TACCTGGTTT TAATAACAGT AAATGTGCCC AGCCTCTTGG      4980

CCCCAGAACT GTACAGTATT GTGGCTGCAC TTGCTCTAAG AGTAGTTGAT GTTGCATTTT      5040

CCTTATTGTT AAAAACATGT TAGAAGCAAT GAATGTATAT AAAAGC                     5086
```

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 717 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..717

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
ATG GCG CAC GCT GGG AGA ACG GGG TAC GAC AAC CGG GAG ATA GTG ATG        48
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
 1               5                  10                  15

AAG TAC ATC CAT TAT AAG CTG TCG CAG AGG GGC TAC GAG TGG GAT GCG        96
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
            20                  25                  30

GGA GAT GTG GGC GCC GCG CCC CCG GGG GCC GCC CCC GCA CCG GGC ATC       144
Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
        35                  40                  45

TTC TCC TCC CAG CCC GGG CAC ACG CCC CAT CCA GCC GCA TCC CGC GAC       192
Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
    50                  55                  60

CCG GTC GCC AGG ACC TCG CCG CTG CAG ACC CCG GCT GCC CCC GGC GCC       240
Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
65                  70                  75                  80

GCC GCG GGG CCT GCG CTC AGC CCG GTG CCA CCT GTG GTC CAC CTG GCC       288
Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
                85                  90                  95

CTC CGC CAA GCC GGC GAC GAC TTC TCC CGC CGC TAC CGC GGC GAC TTC       336
Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
            100                 105                 110

GCC GAG ATG TCC AGC CAG CTG CAC CTG ACG CCC TTC ACC GCG CGG GGA       384
Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
            115                 120                 125

CGC TTT GCC ACG GTG GTG GAG GAG CTC TTC AGG GAC GGG GTG AAC TGG       432
Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
        130                 135                 140

GGG AGG ATT GTG GCC TTC TTT GAG TTC GGT GGG GTC ATG TGT GTG GAG       480
Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145                 150                 155                 160
```

-12-

```
AGC GTC AAC CGG GAG ATG TCG CCC CTG GTG GAC AAC ATC GCC CTG TGG          528
Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
                165                 170                 175

ATG ACT GAG TAC CTG AAC CGG CAC CTG CAC ACC TGG ATC CAG GAT AAC          576
Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
                180                 185                 190

GGA GGC TGG GAT GCC TTT GTG GAA CTG TAC GGC CCC AGC ATG CGG CCT          624
Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
                195                 200                 205

CTG TTT GAT TTC TCC TGG CTG TCT CTG AAG ACT CTG CTC AGT TTG GCC          672
Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
    210                 215                 220

CTG GTG GGA GCT TGC ATC ACC CTG GGT GCC TAT CTG AGC CAC AAG              717
Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Ser His Lys
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:21:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 239 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1               5                   10                  15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
            20              25                  30

Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
        35              40                  45

Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
    50              55                  60

Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
65              70                  75                  80

Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
            85                  90                  95

Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
            100             105             110

Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
            115             120             125

Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
    130             135                 140
```

-13-

```
Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145             150             155             160

Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
            165             170             175

Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
            180             185             190

Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
        195             200             205

Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
    210             215             220

Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Ser His Lys
225             230             235
```

(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 615 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..615

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
ATG GCG CAC GCT GGG AGA ACG GGG TAC GAC AAC CGG GAG ATA GTG ATG        48
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
  1               5                  10                 15

AAG TAC ATC CAT TAT AAG CTG TCG CAG AGG GGC TAC GAG TGG GAT GCG        96
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
                20                  25                 30

GGA GAT GTG GGC GCC GCG CCC CCG GGG GCC GCC CCC GCA CCG GGC ATC       144
Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
                35                  40                 45

TTC TCC TCC CAG CCC GGG CAC ACG CCC CAT CCA GCC GCA TCC CGC GAC       192
Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
        50                  55                  60

CCG GTC GCC AGG ACC TCG CCG CTG CAG ACC CCG GCT GCC CCC GGC GCC       240
Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
 65                 70                  75                  80
```

```
GCC GCG GGG CCT GCG CTC AGC CCG GTG CCA CCT GTG GTC CAC CTG GCC      288
Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
                85                  90                  95

CTC CGC CAA GCC GGC GAC GAC TTC TCC CGC CGC TAC CGC GGC GAC TTC      336
Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
                100                 105                 110

GCC GAG ATG TCC AGC CAG CTG CAC CTG ACG CCC TTC ACC GCG CGG GGA      384
Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
            115                 120                 125

CGC TTT GCC ACG GTG GTG GAG GAG CTC TTC AGG GAC GGG GTG AAC TGG      432
Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
    130                 135                 140

GGG AGG ATT GTG GCC TTC TTT GAG TTC GGT GGG GTC ATG TGT GTG GAG      480
Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145                 150                 155                 160

AGC GTC AAC CGG GAG ATG TCG CCC CTG GTG GAC AAC ATC GCC CTG TGG      528
Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
                165                 170                 175

ATG ACT GAG TAC CTG AAC CGG CAC CTG CAC ACC TGG ATC CAG GAT AAC      576
Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
                180                 185                 190

GGA GGC TGG GTA GGT GCA TCT GGT GAT GTG AGT CTG GGC                  615
Gly Gly Trp Val Gly Ala Ser Gly Asp Val Ser Leu Gly
            195                 200                 205
```

(2)  INFORMATION FOR SEQ ID NO:23:

      (i)  SEQUENCE CHARACTERISTICS:
         (A)  LENGTH: 205 amino acids
         (B)  TYPE: amino acid
         (D)  TOPOLOGY: linear

      (ii)  MOLECULE TYPE: protein

      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1                   5                   10                  15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
                20                  25                  30

Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
                35                  40                  45

Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
    50                  55                  60

Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
65                  70                  75                  80
```

-15-

```
Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
                85                90                95

Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
               100             105             110

Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
           115                 120             125

Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
       130             135             140

Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145             150             155             160

Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
               165             170             175

Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
               180             185             190

Gly Gly Trp Val Gly Ala Ser Gly Asp Val Ser Leu Gly
           195             200             205


(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: Other nucleic acid;
        (A) DESCRIPTION: Synthetic DNA

   (iv) ANTI-SENSE: YES

   (ix) FEATURE:
        (A) NAME/KEY: Modified_base
        (B) LOCATION: 16..17
        (D) OTHER INFORMATION: Last two internucleoside linkages are
            phosphorothioates

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCTCCCAGCG TGCGCCAT                                               18


(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
```

(ii) MOLECULE TYPE: Other nucleic acid;
            (A) DESCRIPTION: Synthetic DNA

       (iv) ANTI-SENSE: NO

       (ix) FEATURE:
            (A) NAME/KEY: Modified_base
            (B) LOCATION: 16..17
            (D) OTHER INFORMATION: Last two internucleoside linkages are
                phosphorothioates

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGCACTCACG CTCGGCCT                                                        18


(2) INFORMATION FOR SEQ ID NO:26:

       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: Other nucleic acid;
            (A) DESCRIPTION: Synthetic DNA

       (iv) ANTI-SENSE: YES

       (ix) FEATURE:
            (A) NAME/KEY: Modified_base
            (B) LOCATION: 18..19
            (D) OTHER INFORMATION: Last two internucleoside linkages are
                phosphorothioates

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCGCGGCGGG CGGGCGGGCA                                                      20


(2) INFORMATION FOR SEQ ID NO:27:

       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: Other nucleic acid;
            (A) DESCRIPTION: Synthetic DNA

       (iv) ANTI-SENSE: NO

       (ix) FEATURE:
            (A) NAME/KEY: Modified_base
            (B) LOCATION: 18..19
            (D) OTHER INFORMATION: Last two internucleoside linkages are
                phosphorothioates

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGGCGGAGGC CGGCCGGCGG                                                    20


(2) INFORMATION FOR SEQ ID NO:28:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Other nucleic acid;
        (A) DESCRIPTION: Synthetic DNA

    (iv) ANTI-SENSE: YES

    (ix) FEATURE:
        (A) NAME/KEY: Modified_base
        (B) LOCATION: 18..19
        (D) OTHER INFORMATION: Last two internucleoside linkages are
            phosphorothioates

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCGGCGGCG GCGGCAGCGC                                                    20


(2) INFORMATION FOR SEQ ID NO:29:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Other nucleic acid;
        (A) DESCRIPTION: Synthetic DNA

    (iv) ANTI-SENSE: NO

    (ix) FEATURE:
        (A) NAME/KEY: Modified_base
        (B) LOCATION: 18..19
        (D) OTHER INFORMATION: Last two internucleoside linkages are
            phosphorothioates

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGCCGGGAA GGGCGCCCGC                                                    20